SEQUENCE LISTING

<110> Bennett, Robert P.
Welch, Peter J.
Harwood, Steven
Madden, Knut
Frimpong, Kenneth
Franke, Kenneth E.

<120> Viral Vectors Containing Recombination Sites

<130> 0942.5450007

<140> US 10/622,088
<141> 2003-07-18

<150> PCT/US03/22437
<151> 2003-07-18

<150> US 60/396,335
<151> 2002-07-18

<150> US 60/398,617
<151> 2002-07-26

<150> US 60/427,231
<151> 2002-11-19

<150> US 60/456,496
<151> 2003-03-24

<150> US 60/474,940
<151> 2003-06-03

<160> 164

<170> PatentIn version 3.2

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ttttacgttt ctcgttcagc ttttttgtac aaagttggca ttataaaaaa gcattgctca   180

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<223>  n may be any nucleotide

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caactttnnn nnnnaaacaa g                                    21


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<400>  45
taatacgact cactataggg                                      20


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accgaggaga gggttaggga t                                    21
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gactttgacc gtttacgtgg agac   24

<210> 48
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<220>
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<400> 48
ccttaagcca cgcccacaca tttc   24

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<400> 49

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
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<400> 50

His His His His His His
1   5

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cggaacaagg gcatgaccaa aatcccttaa cg   32

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gactcaaagg gcttgcttgt gtgttcctta ttg   33

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gttccgaagg gttgtgtcac gtaggccaga taac   34

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gttccgaagg gaataatcga tttaagggtg taatactc   38

<210> 56
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<400> 56
gactcaaagg gtttgcttat tggcaggctc tcc   33

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<210>   58
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<220>
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agatctgggg aagcctatcc ctaaccc                                                27


<210>   62
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<220>
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<210>   63
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aattgatccc ttcaccgaca tagtacag                                          28


<210>   64
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<212>   DNA
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ggtgaaggga tc                                                           12


<210>   65
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<223>   Topo D6 oligonucletide

<400>   65
tcgagcccttt gacatagtac ag                                               22


<210>   66
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<220>
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<400>   66
cgcaaatggg cggtaggcgt g                                                 21


<210>   67
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accgaggaga gggttaggga t                                          21


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tcagtgttag actagtaaat tg                                         22


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<400>   69
atgggatctg ataaa                                                 15


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<400>   70
caccatggga tctgataaa                                             19


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<223>   DNA sequence of the C terminus of a theoretical protein

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aagtcggagc actcgacgac ggtgtag                                    27


<210>   72
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<400>  73                                                              33
gcggttaagt cggagcactc gacgactgca tag


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tgcagtcgtc gagtgctccg actt


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<211>  27
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<213>  Unknown

<220>
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       protein in frame with the C terminal tag in pLenti6 V5 D TOPO

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ctatgcagtc gtcgagtgct ccgactt


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ctgctacgcc ccgccctgc   19

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gtgtgcgccg gtgtacacag gaagtgacaa ttttcgcgcg gttttaggcg gatgttgtag    240

taaatttggg cgtaaccgag taagatttgg ccattttcgc gggaaaactg aataagagga    300

agtgaaatct gaataatttt gtgttactca tagcgcgtaa tatttgtcta gggccgcggg    360

gactttgacc gtttacgtgg agactcgccc aggtgttttt ctcaggtgtt ttccgcgttc    420

cgggtcaaag ttggcgtttt attattatag tcagtcgaag cttggatccg gtacctctag    480

aattctcgag cggccgctag cgacatcgga tctcccgatc ccctatggtc gactctcagt    540

acaatctgct ctgatgccgc atagttaagc cagtatctgc tccctgcttg tgtgttggag    600

gtcgctgagt agtgcgcgag caaaatttaa gctacaacaa ggcaaggctt gaccgacaat    660

tgcatgaaga atctgcttag ggttaggcgt tttgcgctgc ttcgcgatgt acgggccaga    720

tatacgcgtt gacattgatt attgactagt tattaatagt aatcaattac ggggtcatta    780

gttcatagcc catatatgga gttccgcgtt acataactta cggtaaatgg cccgcctggc    840

tgaccgccca cgacccccg cccattgacg tcaataatga cgtatgttcc catagtaacg    900

ccaataggga ctttccattg acgtcaatgg gtggactatt tacggtaaac tgcccacttg    960

gcagtacatc aagtgtatca tatgccaagt acgccccta ttgacgtcaa tgacggtaaa    1020

tggcccgcct ggcattatgc ccagtacatg accttatggg actttcctac ttggcagtac    1080
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ttgacgcaaa  tgggcggtag  gcgtgtacgg  tgggaggtct  atataagcag  agctctctgg    1320

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aaaatgatat  aaatatcaat  atattaaatt  agattttgca  taaaaaacag  actacataat    1500

actgtaaaac  acaacatatc  cagtcactat  gaatcaacta  cttagatggt  attagtgacc    1560

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tgtaattcat  taagcattct  gccgacatgg  aagccatcac  agacggcatg  atgaacctga    2700

atcgccagcg  gcatcagcac  cttgtcgcct  tgcgtataat  atttgcccat  ggtgaaaacg    2760

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acacgacggg gagtcaggca actatggatg aacgaaatag acagatcgct gagataggtg    4920

cctcactgat taagcattgg taactgtcag accaagttta ctcatatata ctttagattg    4980

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caaaaaagct gaacgagaaa cgtaaaatga tataaatatc aatatattaa attagatttt     180

gcataaaaaa cagactacat aatactgtaa aacacaacat atccagtcac tatggcggcc     240

gctccctaac ccacggggcc cgtggctatg cagggcttg ccgccccgac gttggctgcg      300

agccctgggc cttcacccga acttgggggt tggggtgggg aaaaggaaga aacgcgggcg     360

tattggtccc aatggggtct cggtggggta tcgacagagt gccagccctg gaccgaacc      420

ccgcgtttat gaacaaacga cccaacaccc gtgcgtttta ttctgtcttt ttattgccgt     480

catagcgcgg gttccttccg gtattgtctc cttccgtgtt tcagttagcc tcccccatct     540

cccgggcaaa cgtgcgcgcc aggtcgcaga tcgtcggtat ggagcctggg gtggtgacgt     600

gggtctggac catcccggag gtaagttgca gcagggcgtc ccggcagccg gcgggcgatt     660

ggtcgtaatc caggataaag acatgcatgg gacggaggcg tttggccaag acgtccaaag     720
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cccaggcaaa cacgttatac aggtcgccgt tgggggccag caactcgggg gcccgaaaca    780

gggtaaataa cgtgtccccg atatggggtc gtgggcccgc gttgctctgg ggctcggcac    840

cctggggcgg cacggccgcc cccgaaagct gtccccaatc ctcccgccac gacccgccgc    900

cctgcagata ccgcaccgta ttggcaagca gcccataaac gcggcgaatc gcggccagca    960

tagccaggtc aagccgctcg ccggggcgct ggcgtttggc caggcggtcg atgtgtctgt    1020

cctccggaag ggcccccaac acgatgtttg tgccgggcaa ggtcggcggg atgagggcca    1080

cgaacgccag cacggcctgg ggggtcatgc tgcccataag gtatcgcgcg gccgggtagc    1140

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gtgagctccc agcctccccc ccgatatgag gagccagaac ggcgtcggtc acggcataag    1260

gcatgcccat tgttatctgg gcgcttgtca ttaccaccgc cgcgtccccg gccgatatct    1320

caccctggtc gaggcggtgt tgtgtggtgt agatgttcgc gattgtctcg gaagccccca    1380

acacccgcca gtaagtcatc ggctcgggta cgtagacgat atcgtcgcgc gaacccaggg    1440

ccaccagcag ttgcgtggtg gtggtttttcc ccatcccgtg gggaccgtct atataaaccc    1500

gcagtagcgt gggcattttc tgctccaggc ggacttccgt ggcttttttgt tgccggcgag    1560

ggcgcaacgc cgtacgtcgg ttgttatggc cgcgagaacg cgcagcctgg tcgaacgcag    1620

acgcgtgttg atggcagggg tacgaagcca tagatcccgt tatcaattac ttatactatc    1680

cggcgcgcaa gcgagcgtgt gcgccggagc acaattgata ctgatttacg agttgggcaa    1740

acgggcttta tatagcctgt cccctccaca gccctagtgc cgtgcgcaaa gtgcctacgt    1800

gaccaggctc tcctacgcat atacaatctt atctctatag ataaggtttc catatataaa    1860

gcctctcgat ggctgaacgt gcacagtatc gtgttgattt ctgagtgcta actaacagtt    1920

acaatgaacc gtttttttcg agagaataac atttttgacg cgccaaggac cggggggcaag    1980

ggtcgtgcca aatctttgcc agcgcctgcc gccaactcgc cgccgtcgcc tgttcgtccg    2040

ccgccaaaat ctaacatcaa accacctacg cgcatctctc cgcctaaaca gcctatgtgc    2100

acctctccgg ccaagccgtt ggagcacagc agcattgtaa gtaaaaaacc agtcgtcaac    2160

agaaagatg gatattttgt ccgcccgag tttgggaaca agtttgaagg tttgcccgcg    2220

tacagcgaca aactggattt caaacaagag cgcgatctac gtacctgcag gcccgggctc    2280

aacccaacac aatatattat agttaaataa gaattattat caaatcattt gtatattaat    2340

taaaatacta tactgtaaat tacatttttat ttacaattca ctctaga atg acc atg    2396
                                                        Met Thr Met
                                                        1

att acg gat tca ctg gcc gtc gtt tta caa cgt cgt gac tgg gaa aac    2444
Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Arg Asp Trp Glu Asn
     5                   10                  15
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```
cct ggc gtt acc caa ctt aat cgc ctt gca gca cat ccc cct ttc gcc    2492
Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro Pro Phe Ala
20              25              30              35

agc tgg cgt aat agc gaa gag gcc cgc acc gat cgc cct tcc caa cag    2540
Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln
                40              45              50

ttg cgc agc ctg aat ggc gaa tgg cgc ttt gcc tgg ttt ccg gca cca    2588
Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe Pro Ala Pro
                55              60              65

gaa gcg gtg ccg gaa agc tgg ctg gag tgc gat ctt cct gag gcc gat    2636
Glu Ala Val Pro Glu Ser Trp Leu Glu Cys Asp Leu Pro Glu Ala Asp
            70              75              80

act gtc gtc gtc ccc tca aac tgg cag atg cac ggt tac gat gcg ccc    2684
Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr Asp Ala Pro
            85              90              95

atc tac acc aac gta acc tat ccc att acg gtc aat ccg ccg ttt gtt    2732
Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro Pro Phe Val
100             105             110             115

ccc acg gag aat ccg acg ggt tgt tac tcg ctc aca ttt aat gtt gat    2780
Pro Thr Glu Asn Pro Thr Gly Cys Tyr Ser Leu Thr Phe Asn Val Asp
                120             125             130

gaa agc tgg cta cag gaa ggc cag acg cga att att ttt gat ggc gtt    2828
Glu Ser Trp Leu Gln Glu Gly Gln Thr Arg Ile Ile Phe Asp Gly Val
                135             140             145

aac tcg gcg ttt cat ctg tgg tgc aac ggg cgc tgg gtc ggt tac ggc    2876
Asn Ser Ala Phe His Leu Trp Cys Asn Gly Arg Trp Val Gly Tyr Gly
            150             155             160

cag gac agt cgt ttg ccg tct gaa ttt gac ctg agc gca ttt tta cgc    2924
Gln Asp Ser Arg Leu Pro Ser Glu Phe Asp Leu Ser Ala Phe Leu Arg
            165             170             175

gcc gga gaa aac cgc ctc gcg gtg atg gtg ctg cgt tgg agt gac ggc    2972
Ala Gly Glu Asn Arg Leu Ala Val Met Val Leu Arg Trp Ser Asp Gly
180             185             190             195

agt tat ctg gaa gat cag gat atg tgg cgg atg agc ggc att ttc cgt    3020
Ser Tyr Leu Glu Asp Gln Asp Met Trp Arg Met Ser Gly Ile Phe Arg
                200             205             210

gac gtc tcg ttg ctg cat aaa ccg act aca caa atc agc gat ttc cat    3068
Asp Val Ser Leu Leu His Lys Pro Thr Thr Gln Ile Ser Asp Phe His
                215             220             225

gtt gcc act cgc ttt aat gat gat ttc agc cgc gct gta ctg gag gct    3116
Val Ala Thr Arg Phe Asn Asp Asp Phe Ser Arg Ala Val Leu Glu Ala
            230             235             240

gaa gtt cag atg tgc ggc gag ttg cgt gac tac cta cgg gta aca gtt    3164
Glu Val Gln Met Cys Gly Glu Leu Arg Asp Tyr Leu Arg Val Thr Val
245             250             255
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tct tta tgg cag ggt gaa acg cag gtc gcc agc ggc acc gcg cct ttc        3212
Ser Leu Trp Gln Gly Glu Thr Gln Val Ala Ser Gly Thr Ala Pro Phe
260             265                 270                 275

ggc ggt gaa att atc gat gag cgt ggt ggt tat gcc gat cgc gtc aca        3260
Gly Gly Glu Ile Ile Asp Glu Arg Gly Gly Tyr Ala Asp Arg Val Thr
                280                 285                 290

cta cgt ctg aac gtc gaa aac ccg aaa ctg tgg agc gcc gaa atc ccg        3308
Leu Arg Leu Asn Val Glu Asn Pro Lys Leu Trp Ser Ala Glu Ile Pro
            295                 300                 305

aat ctc tat cgt gcg gtg gtt gaa ctg cac acc gcc gac ggc acg ctg        3356
Asn Leu Tyr Arg Ala Val Val Glu Leu His Thr Ala Asp Gly Thr Leu
            310                 315                 320

att gaa gca gaa gcc tgc gat gtc ggt ttc cgc gag gtg cgg att gaa        3404
Ile Glu Ala Glu Ala Cys Asp Val Gly Phe Arg Glu Val Arg Ile Glu
        325                 330                 335

aat ggt ctg ctg ctg ctg aac ggc aag ccg ttg ctg att cga ggc gtt        3452
Asn Gly Leu Leu Leu Leu Asn Gly Lys Pro Leu Leu Ile Arg Gly Val
340             345                 350                 355

aac cgt cac gag cat cat cct ctg cat ggt cag gtc atg gat gag cag        3500
Asn Arg His Glu His His Pro Leu His Gly Gln Val Met Asp Glu Gln
                360                 365                 370

acg atg gtg cag gat atc ctg ctg atg aag cag aac aac ttt aac gcc        3548
Thr Met Val Gln Asp Ile Leu Leu Met Lys Gln Asn Asn Phe Asn Ala
                375                 380                 385

gtg cgc tgt tcg cat tat ccg aac cat ccg ctg tgg tac acg ctg tgc        3596
Val Arg Cys Ser His Tyr Pro Asn His Pro Leu Trp Tyr Thr Leu Cys
            390                 395                 400

gac cgc tac ggc ctg tat gtg gtg gat gaa gcc aat att gaa acc cac        3644
Asp Arg Tyr Gly Leu Tyr Val Val Asp Glu Ala Asn Ile Glu Thr His
            405                 410                 415

ggc atg gtg cca atg aat cgt ctg acc gat gat ccg cgc tgg cta ccg        3692
Gly Met Val Pro Met Asn Arg Leu Thr Asp Asp Pro Arg Trp Leu Pro
420             425                 430                 435

gcg atg agc gaa cgc gta acg cga atg gtg cag cgc gat cgt aat cac        3740
Ala Met Ser Glu Arg Val Thr Arg Met Val Gln Arg Asp Arg Asn His
                440                 445                 450

ccg agt gtg atc atc tgg tcg ctg ggg aat gaa tca ggc cac ggc gct        3788
Pro Ser Val Ile Ile Trp Ser Leu Gly Asn Glu Ser Gly His Gly Ala
            455                 460                 465

aat cac gac gcg ctg tat cgc tgg atc aaa tct gtc gat cct tcc cgc        3836
Asn His Asp Ala Leu Tyr Arg Trp Ile Lys Ser Val Asp Pro Ser Arg
            470                 475                 480

ccg gtg cag tat gaa ggc ggc gga gcc gac acc acg gcc acc gat att        3884
Pro Val Gln Tyr Glu Gly Gly Gly Ala Asp Thr Thr Ala Thr Asp Ile
485                 490                 495

att tgc ccg atg tac gcg cgc gtg gat gaa gac cag ccc ttc ccg gct        3932
Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro Phe Pro Ala
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Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro Phe Pro Ala
500             505             510             515

gtg ccg aaa tgg tcc atc aaa aaa tgg ctt tcg cta cct gga gag acg    3980
Val Pro Lys Trp Ser Ile Lys Lys Trp Leu Ser Leu Pro Gly Glu Thr
                520             525             530

cgc ccg ctg atc ctt tgc gaa tac gcc cac gcg atg ggt aac agt ctt    4028
Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly Asn Ser Leu
                535             540             545

ggc ggt ttc gct aaa tac tgg cag gcg ttt cgt cag tat ccc cgt tta    4076
Gly Gly Phe Ala Lys Tyr Trp Gln Ala Phe Arg Gln Tyr Pro Arg Leu
            550             555             560

cag ggc ggc ttc gtc tgg gac tgg gtg gat cag tcg ctg att aaa tat    4124
Gln Gly Gly Phe Val Trp Asp Trp Val Asp Gln Ser Leu Ile Lys Tyr
        565             570             575

gat gaa aac ggc aac ccg tgg tcg gct tac ggc ggt gat ttt ggc gat    4172
Asp Glu Asn Gly Asn Pro Trp Ser Ala Tyr Gly Gly Asp Phe Gly Asp
580             585             590             595

acg ccg aac gat cgc cag ttc tgt atg aac ggt ctg gtc ttt gcc gac    4220
Thr Pro Asn Asp Arg Gln Phe Cys Met Asn Gly Leu Val Phe Ala Asp
                600             605             610

cgc acg ccg cat cca gcg ctg acg gaa gca aaa cac cag cag cag ttt    4268
Arg Thr Pro His Pro Ala Leu Thr Glu Ala Lys His Gln Gln Gln Phe
                615             620             625

ttc cag ttc cgt tta tcc ggg caa acc atc gaa gtg acc agc gaa tac    4316
Phe Gln Phe Arg Leu Ser Gly Gln Thr Ile Glu Val Thr Ser Glu Tyr
            630             635             640

ctg ttc cgt cat agc gat aac gag ctc ctg cac tgg atg gtg gcg ctg    4364
Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Met Val Ala Leu
        645             650             655

gat ggt aag ccg ctg gca agc ggt gaa gtg cct ctg gat gtc gct cca    4412
Asp Gly Lys Pro Leu Ala Ser Gly Glu Val Pro Leu Asp Val Ala Pro
660             665             670             675

caa ggt aaa cag ttg att gaa ctg cct gaa cta ccg cag ccg gag agc    4460
Gln Gly Lys Gln Leu Ile Glu Leu Pro Glu Leu Pro Gln Pro Glu Ser
                680             685             690

gcc ggg caa ctc tgg ctc aca gta cgc gta gtg caa ccg aac gcg acc    4508
Ala Gly Gln Leu Trp Leu Thr Val Arg Val Val Gln Pro Asn Ala Thr
                695             700             705

gca tgg tca gaa gcc ggg cac atc agc gcc tgg cag cag tgg cgt ctg    4556
Ala Trp Ser Glu Ala Gly His Ile Ser Ala Trp Gln Gln Trp Arg Leu
            710             715             720

gcg gaa aac ctc agt gtg acg ctc ccc gcc gcg tcc cac gcc atc ccg    4604
Ala Glu Asn Leu Ser Val Thr Leu Pro Ala Ala Ser His Ala Ile Pro
        725             730             735

cat ctg acc acc agc gaa atg gat ttt tgc atc gag ctg ggt aat aag    4652
His Leu Thr Thr Ser Glu Met Asp Phe Cys Ile Glu Leu Gly Asn Lys
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       740                          745                         750                         755

cgt tgg caa ttt aac cgc cag tca ggc ttt ctt tca cag atg tgg att      4700
Arg Trp Gln Phe Asn Arg Gln Ser Gly Phe Leu Ser Gln Met Trp Ile
                760                         765                 770

ggc gat aaa aaa caa ctg ctg acg ccg ctg cgc gat cag ttc acc cgt      4748
Gly Asp Lys Lys Gln Leu Leu Thr Pro Leu Arg Asp Gln Phe Thr Arg
                775                         780                 785

gca ccg ctg gat aac gac att ggc gta agt gaa gcg acc cgc att gac      4796
Ala Pro Leu Asp Asn Asp Ile Gly Val Ser Glu Ala Thr Arg Ile Asp
                790                         795                 800

cct aac gcc tgg gtc gaa cgc tgg aag gcg gcg ggc cat tac cag gcc      4844
Pro Asn Ala Trp Val Glu Arg Trp Lys Ala Ala Gly His Tyr Gln Ala
        805                         810                 815

gaa gca gcg ttg ttg cag tgc acg gca gat aca ctt gct gat gcg gtg      4892
Glu Ala Ala Leu Leu Gln Cys Thr Ala Asp Thr Leu Ala Asp Ala Val
820                         825                 830                 835

ctg att acg acc gct cac gcg tgg cag cat cag ggg aaa acc tta ttt      4940
Leu Ile Thr Thr Ala His Ala Trp Gln His Gln Gly Lys Thr Leu Phe
                840                         845                 850

atc agc cgg aaa acc tac cgg att gat ggt agt ggt caa atg gcg att      4988
Ile Ser Arg Lys Thr Tyr Arg Ile Asp Gly Ser Gly Gln Met Ala Ile
                855                         860                 865

acc gtt gat gtt gaa gtg gcg agc gat aca ccg cat ccg gcg cgg att      5036
Thr Val Asp Val Glu Val Ala Ser Asp Thr Pro His Pro Ala Arg Ile
                870                         875                 880

ggc ctg aac tgc cag ctg gcg cag gta gca gag cgg gta aac tgg ctc      5084
Gly Leu Asn Cys Gln Leu Ala Gln Val Ala Glu Arg Val Asn Trp Leu
        885                         890                 895

gga tta ggg ccg caa gaa aac tat ccc gac cgc ctt act gcc gcc tgt      5132
Gly Leu Gly Pro Gln Glu Asn Tyr Pro Asp Arg Leu Thr Ala Ala Cys
900                         905                         910                 915

ttt gac cgc tgg gat ctg cca ttg tca gac atg tat acc ccg tac gtc      5180
Phe Asp Arg Trp Asp Leu Pro Leu Ser Asp Met Tyr Thr Pro Tyr Val
                        920                         925                 930

ttc ccg agc gaa aac ggt ctg cgc tgc ggg acg cgc gaa ttg aat tat      5228
Phe Pro Ser Glu Asn Gly Leu Arg Cys Gly Thr Arg Glu Leu Asn Tyr
                935                         940                 945

ggc cca cac cag tgg cgc ggc gac ttc cag ttc aac atc agc cgc tac      5276
Gly Pro His Gln Trp Arg Gly Asp Phe Gln Phe Asn Ile Ser Arg Tyr
                950                         955                 960

agt caa cag caa ctg atg gaa acc agc cat cgc cat ctg ctg cac gcg      5324
Ser Gln Gln Gln Leu Met Glu Thr Ser His Arg His Leu Leu His Ala
        965                         970                 975

gaa gaa ggc aca tgg ctg aat atc gac ggt ttc cat atg ggg att ggt      5372
Glu Glu Gly Thr Trp Leu Asn Ile Asp Gly Phe His Met Gly Ile Gly
980                         985                         990                 995
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ggc gac gac tcc tgg   agc ccg tca gta tcg   gcg gaa ttc cag ctg        5417
Gly Asp Asp Ser Trp   Ser Pro Ser Val Ser   Ala Glu Phe Gln Leu
            1000                 1005                      1010

agc gcc ggt cgc tac   cat tac cag ttg gtc   tgg tgt caa aaa taa        5462
Ser Ala Gly Arg Tyr   His Tyr Gln Leu Val   Trp Cys Gln Lys
            1015                 1020

tgactgcagg tcgaccatag tgactggata tgttgtgttt tacagtatta tgtagtctgt      5522

tttttatgca aaatctaatt taatatattg atatttatat cattttacgt ttctcgttca      5582

gctttcttgt acaaagtggt gagaatgaat gaagatctg ggg   aag cct atc cct       5636
                                             Gly   Lys Pro Ile Pro
                                                        1025

aac   cct ctc ctc ggt ctc   gat tct acg cgt acc   ggt cat cat cac      5681
Asn   Pro Leu Leu Gly Leu   Asp Ser Thr Arg Thr   Gly His His His
1030                1035                 1040
                                                                       5693

cat   cac cat tga
His   His His
1045
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<212>   PRT
<213>   Artificial Sequence

<220>
<223>   V5-His DEST cassette

<400>   91

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Arg Asp
1               5                   10                  15


Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
            20                  25                  30


Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro
            35                  40                  45


Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe
            50                  55                  60


Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu Glu Cys Asp Leu Pro
65                  70                  75                  80


Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
                85                  90                  95


Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro
```

```
                100                    105                    110


Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys Tyr Ser Leu Thr Phe
        115                 120             125


Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln Thr Arg Ile Ile Phe
    130                 135                 140


Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn Gly Arg Trp Val
145                 150                 155                 160


Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu Phe Asp Leu Ser Ala
                165                 170                 175


Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val Met Val Leu Arg Trp
            180                 185                 190


Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp Arg Met Ser Gly
        195                 200                 205


Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro Thr Thr Gln Ile Ser
    210                 215                 220


Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp Phe Ser Arg Ala Val
225                 230                 235                 240


Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu Arg Asp Tyr Leu Arg
                245                 250                 255


Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln Val Ala Ser Gly Thr
            260                 265                 270


Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg Gly Gly Tyr Ala Asp
        275                 280                 285


Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro Lys Leu Trp Ser Ala
    290                 295                 300


Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu Leu His Thr Ala Asp
305                 310                 315                 320


Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val Gly Phe Arg Glu Val
                325                 330                 335


Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly Lys Pro Leu Leu Ile
            340                 345                 350
```

Arg Gly Val Asn Arg His Glu His His Pro Leu His Gly Gln Val Met
    355   360   365

Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu Met Lys Gln Asn Asn
    370   375   380

Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn His Pro Leu Trp Tyr
385   390   395   400

Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val Asp Glu Ala Asn Ile
            405   410   415

Glu Thr His Gly Met Val Pro Met Asn Arg Leu Thr Asp Asp Pro Arg
        420   425   430

Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg Met Val Gln Arg Asp
        435   440   445

Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu Gly Asn Glu Ser Gly
    450   455   460

His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp Ile Lys Ser Val Asp
465   470   475   480

Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly Ala Asp Thr Thr Ala
            485   490   495

Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro
        500   505   510

Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys Trp Leu Ser Leu Pro
        515   520   525

Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly
    530   535   540

Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln Ala Phe Arg Gln Tyr
545   550   555   560

Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp Val Asp Gln Ser Leu
            565   570   575

Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala Tyr Gly Gly Asp
        580   585   590

Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met Asn Gly Leu Val
     595   600   605

Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu Ala Lys His Gln
     610   615   620

Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr Ile Glu Val Thr
625   630   635   640

Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Met
          645   650   655

Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu Val Pro Leu Asp
          660   665   670

Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu Pro Glu Leu Pro Gln
          675   680   685

Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val Arg Val Val Gln Pro
     690   695   700

Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile Ser Ala Trp Gln Gln
705   710   715   720

Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu Pro Ala Ala Ser His
          725   730   735

Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp Phe Cys Ile Glu Leu
          740   745   750

Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser Gly Phe Leu Ser Gln
          755   760   765

Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr Pro Leu Arg Asp Gln
     770   775   780

Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly Val Ser Glu Ala Thr
785   790   795   800

Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp Lys Ala Ala Gly His
          805   810   815

Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr Ala Asp Thr Leu Ala
          820   825   830

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Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp Gln His Gln Gly Lys
        835                 840                 845

Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile Asp Gly Ser Gly Gln
    850                 855                 860

Met Ala Ile Thr Val Asp Val Glu Val Ala Ser Asp Thr Pro His Pro
865                 870                 875                 880

Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln Val Ala Glu Arg Val
            885                 890                 895

Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr Pro Asp Arg Leu Thr
            900                 905                 910

Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu Ser Asp Met Tyr Thr
            915                 920                 925

Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg Cys Gly Thr Arg Glu
    930                 935                 940

Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp Phe Gln Phe Asn Ile
945                 950                 955                 960

Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser His Arg His Leu
            965                 970                 975

Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile Asp Gly Phe His Met
            980                 985                 990

Gly Ile Gly Gly Asp Asp Ser Trp  Ser Pro Ser Val Ser  Ala Glu Phe
    995                 1000                1005

Gln Leu  Ser Ala Gly Arg Tyr  His Tyr Gln Leu Val  Trp Cys Gln
    1010                1015                1020

Lys
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<210>  92
<211>  23
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  V5-His DEST cassette

<400>  92
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```
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
1               5                   10                  15


Gly His His His His His
            20


<210>   93
<211>   376
<212>   PRT
<213>   Herpesvirus sp.

<400>   93

Met Ala Ser Tyr Pro Cys His Gln His Ala Ser Ala Phe Asp Gln Ala
1               5                   10                  15


Ala Arg Ser Arg Gly His Asn Asn Arg Arg Thr Ala Leu Arg Pro Arg
            20                  25                  30


Arg Gln Gln Lys Ala Thr Glu Val Arg Leu Glu Gln Lys Met Pro Thr
            35                  40                  45


Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys Thr Thr
    50                  55                  60


Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg Asp Asp Ile Val Tyr
65                  70                  75                  80


Val Pro Glu Pro Met Thr Tyr Trp Arg Val Leu Gly Ala Ser Glu Thr
                85                  90                  95


Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln Gly Glu Ile
                100                 105                 110


Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala Gln Ile Thr Met
            115                 120                 125


Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu Ala Pro His Ile Gly
    130                 135                 140


Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro Ala Leu Thr Leu Ile
145                 150                 155                 160


Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala Arg
                165                 170                 175


Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val Leu Ala Phe Val Ala
```

```
                  180                    185                    190


Leu Ile Pro Pro Thr Leu Pro Gly Thr Asn Ile Val Leu Gly Ala Leu
        195                 200                 205


Pro Glu Asp Arg His Ile Asp Arg Leu Ala Lys Arg Gln Arg Pro Gly
    210                 215                 220


Glu Arg Leu Asp Leu Ala Met Leu Ala Ala Ile Arg Arg Val Tyr Gly
225                 230                 235                 240


Leu Leu Ala Asn Thr Val Arg Tyr Leu Gln Gly Gly Gly Ser Trp Arg
            245                 250                 255


Glu Asp Trp Gly Gln Leu Ser Gly Ala Ala Val Pro Pro Gln Gly Ala
            260                 265                 270


Glu Pro Gln Ser Asn Ala Gly Pro Arg Pro His Ile Gly Asp Thr Leu
        275                 280                 285


Phe Thr Leu Phe Arg Ala Pro Glu Leu Leu Ala Pro Asn Gly Asp Leu
    290                 295                 300


Tyr Asn Val Phe Ala Trp Ala Leu Asp Val Leu Ala Lys Arg Leu Arg
305                 310                 315                 320


Pro Met His Val Phe Ile Leu Asp Tyr Asp Gln Ser Pro Ala Gly Cys
            325                 330                 335


Arg Asp Ala Leu Leu Gln Leu Thr Ser Gly Met Val Gln Thr His Val
            340                 345                 350


Thr Thr Pro Gly Ser Ile Pro Thr Ile Cys Asp Leu Ala Arg Thr Phe
        355                 360                 365


Ala Arg Glu Met Gly Glu Ala Asn
    370                 375
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<210> 94
<211> 5763
<212> DNA
<213> Artificial Sequence

<220>
<223> Mel/V5-His DEST cassette

<220>

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<221>  CDS
<222>  (102)..(164)

<220>
<221>  gene
<222>  (591)..(1770)

<220>
<221>  CDS
<222>  (2458)..(5532)

<220>
<221>  CDS
<222>  (5692)..(5763)

<400>  94
ataagtattt tactgttttc gtaacagttt tgtaataaaa aaacctataa atattccgga      60

ttattcatac cgtcccacca tcgggcgcgg atcctataaa t atg aaa ttc tta gtc     116
                                              Met Lys Phe Leu Val
                                               1               5

aac gtt gcc ctt gtt ttt atg gtc gta tac att tct tac atc tat gcg      164
Asn Val Ala Leu Val Phe Met Val Val Tyr Ile Ser Tyr Ile Tyr Ala
             10                  15                  20

gcatggtcga atcaaacaag tttgtacaaa aaagctgaac gagaaacgta aaatgatata     224

aatatcaata tattaaatta gattttgcat aaaaaacaga ctacataata ctgtaaaaca     284

caacatatcc agtcactatg gcggccgctc cctaacccac ggggcccgtg gctatggcag     344

ggcttgccgc cccgacgttg gctgcgagcc ctgggccttc acccgaactt gggggttggg     404

gtggggaaaa ggaagaaacg cgggcgtatt ggtcccaatg gggtctcggt ggggtatcga     464

cagagtgcca gccctgggac cgaaccccgc gtttatgaac aaacgaccca acacccgtgc     524

gttttattct gtcttttttat tgccgtcata gcgcgggttc cttccggtat tgtctccttc    584

cgtgtttcag ttagcctccc ccatctcccg ggcaaacgtg cgcgccaggt cgcagatcgt     644

cggtatggag cctggggtgg tgacgtgggt ctggaccatc ccggaggtaa gttgcagcag     704

ggcgtcccgg cagccggcgg gcgattggtc gtaatccagg ataaagacat gcatgggacg     764

gaggcgtttg gccaagacgt ccaaagccca ggcaaacacg ttatacaggt cgccgttggg     824

ggccagcaac tcgggggccc gaaacagggt aaataacgtg tccccgatat ggggtcgtgg     884

gcccgcgttg ctctggggct cggcaccctg gggcggcacg ccgcccccg aaagctgtcc      944

ccaatcctcc cgccacgacc cgccgccctg cagataccgc accgtattgg caagcagccc    1004

ataaacgcgg cgaatcgcgg ccagcatagc caggtcaagc cgctcgccgg ggcgctggcg    1064

tttggccagg cggtcgatgt gtctgtcctc cggaagggcc cccaacacga tgtttgtgcc    1124

gggcaaggtc ggcgggatga gggccacgaa cgccagcacg gcctggggggg tcatgctgcc   1184

cataaggtat cgcgcggccg ggtagcacag gagggcggcg atgggatggc ggtcgaagat    1244
```

```
gagggtgagg gccggggggcg gggcatgtga gctcccagcc tccccccccga tatgaggagc   1304

cagaacggcg tcggtcacgg cataaggcat gcccattgtt atctgggcgc ttgtcattac   1364

caccgccgcg tccccggccg atatctcacc ctggtcgagg cggtgttgtg tggtgtagat   1424

gttcgcgatt gtctcggaag cccccaacac ccgccagtaa gtcatcggct cgggtacgta   1484

gacgatatcg tcgcgcgaac ccagggccac cagcagttgc gtggtggtgg ttttccccat   1544

cccgtgggga ccgtctatat aaacccgcag tagcgtgggc attttctgct ccaggcggac   1604

ttccgtggct ttttgttgcc ggcgagggcg caacgccgta cgtcggttgt tatggccgcg   1664

agaacgcgca gcctggtcga acgcagacgc gtgttgatgg caggggtacg aagccataga   1724

tcccgttatc aattacttat actatccggc gcgcaagcga gcgtgtgcgc cggagcacaa   1784

ttgatactga tttacgagtt gggcaaacgg gctttatata gcctgtcccc tccacagccc   1844

tagtgccgtg cgcaaagtgc ctacgtgacc aggctctcct acgcatatac aatcttatct   1904

ctatagataa ggtttccata tataaagcct ctcgatggct gaacgtgcac agtatcgtgt   1964

tgatttctga gtgctaacta acagttacaa tgaaccgttt ttttcgagag aataacattt   2024

ttgacgcgcc aaggaccggg ggcaagggtc gtgccaaatc tttgccagcg cctgccgcca   2084

actcgccgcc gtcgcctgtt cgtccgccgc caaaatctaa catcaaacca cctacgcgca   2144

tctctccgcc taaacagcct atgtgcacct ctccggccaa gccgttggag cacagcagca   2204

ttgtaagtaa aaaaccagtc gtcaacagaa aagatggata ttttgtgccg cccgagtttg   2264

ggaacaagtt tgaaggtttg cccgcgtaca gcgacaaact ggatttcaaa caagagcgcg   2324

atctacgtac ctgcaggccc gggctcaacc caacacaata tattatagtt aaataagaat   2384

tattatcaaa tcatttgtat attaattaaa atactatact gtaaattaca ttttatttac   2444
```

```
aattcactct aga atg acc atg att acg gat tca ctg gcc gtc gtt tta       2493
            Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu
                     25                  30
```

```
caa cgt cgt gac tgg gaa aac cct ggc gtt acc caa ctt aat cgc ctt      2541
Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu
 35              40                  45
```

```
gca gca cat ccc cct ttc gcc agc tgg cgt aat agc gaa gag gcc cgc      2589
Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg
 50              55                  60                  65
```

```
acc gat cgc cct tcc caa cag ttg cgc agc ctg aat ggc gaa tgg cgc      2637
Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg
                 70                  75                  80
```

```
ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gaa agc tgg ctg gag      2685
Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu Glu
             85                  90                  95
```

```
tgc gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac tgg cag        2733
Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln
        100                 105                 110

atg cac ggt tac gat gcg ccc atc tac acc aac gta acc tat ccc att        2781
Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile
        115                 120                 125

acg gtc aat ccg ccg ttt gtt ccc acg gag aat ccg acg ggt tgt tac        2829
Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys Tyr
130                 135                 140                 145

tcg ctc aca ttt aat gtt gat gaa agc tgg cta cag gaa ggc cag acg        2877
Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln Thr
                150                 155                 160

cga att att ttt gat ggc gtt aac tcg gcg ttt cat ctg tgg tgc aac        2925
Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn
                165                 170                 175

ggg cgc tgg gtc ggt tac ggc cag gac agt cgt ttg ccg tct gaa ttt        2973
Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu Phe
                180                 185                 190

gac ctg agc gca ttt tta cgc gcc gga gaa aac cgc ctc gcg gtg atg        3021
Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val Met
        195                 200                 205

gtg ctg cgt tgg agt gac ggc agt tat ctg gaa gat cag gat atg tgg        3069
Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp
210                 215                 220                 225

cgg atg agc ggc att ttc cgt gac gtc tcg ttg ctg cat aaa ccg act        3117
Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro Thr
                230                 235                 240

aca caa atc agc gat ttc cat gtt gcc act cgc ttt aat gat gat ttc        3165
Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp Phe
                245                 250                 255

agc cgc gct gta ctg gag gct gaa gtt cag atg tgc ggc gag ttg cgt        3213
Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu Arg
        260                 265                 270

gac tac cta cgg gta aca gtt tct tta tgg cag ggt gaa acg cag gtc        3261
Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln Val
        275                 280                 285

gcc agc ggc acc gcg cct ttc ggc ggt gaa att atc gat gag cgt ggt        3309
Ala Ser Gly Thr Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg Gly
290                 295                 300                 305

ggt tat gcc gat cgc gtc aca cta cgt ctg aac gtc gaa aac ccg aaa        3357
Gly Tyr Ala Asp Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro Lys
                310                 315                 320

ctg tgg agc gcc gaa atc ccg aat ctc tat cgt gcg gtg gtt gaa ctg        3405
Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu Leu
        325                 330                 335

cac acc gcc gac ggc acg ctg att gaa gca gaa gcc tgc gat gtc ggt        3453
His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val Gly
```

```
His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val Gly
    340                 345                 350

ttc cgc gag gtg cgg att gaa aat ggt ctg ctg ctg ctg aac ggc aag    3501
Phe Arg Glu Val Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly Lys
    355                 360                 365

ccg ttg ctg att cga ggc gtt aac cgt cac gag cat cat cct ctg cat    3549
Pro Leu Leu Ile Arg Gly Val Asn Arg His Glu His His Pro Leu His
370                 375                 380                 385

ggt cag gtc atg gat gag cag acg atg gtg cag gat atc ctg ctg atg    3597
Gly Gln Val Met Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu Met
                390                 395                 400

aag cag aac aac ttt aac gcc gtg cgc tgt tcg cat tat ccg aac cat    3645
Lys Gln Asn Asn Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn His
            405                 410                 415

ccg ctg tgg tac acg ctg tgc gac cgc tac ggc ctg tat gtg gtg gat    3693
Pro Leu Trp Tyr Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val Asp
        420                 425                 430

gaa gcc aat att gaa acc cac ggc atg gtg cca atg aat cgt ctg acc    3741
Glu Ala Asn Ile Glu Thr His Gly Met Val Pro Met Asn Arg Leu Thr
    435                 440                 445

gat gat ccg cgc tgg cta ccg gcg atg agc gaa cgc gta acg cga atg    3789
Asp Asp Pro Arg Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg Met
450                 455                 460                 465

gtg cag cgc gat cgt aat cac ccg agt gtg atc atc tgg tcg ctg ggg    3837
Val Gln Arg Asp Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu Gly
                470                 475                 480

aat gaa tca ggc cac ggc gct aat cac gac gcg ctg tat cgc tgg atc    3885
Asn Glu Ser Gly His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp Ile
            485                 490                 495

aaa tct gtc gat cct tcc cgc ccg gtg cag tat gaa ggc ggc gga gcc    3933
Lys Ser Val Asp Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly Ala
        500                 505                 510

gac acc acg gcc acc gat att att tgc ccg atg tac gcg cgc gtg gat    3981
Asp Thr Thr Ala Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val Asp
    515                 520                 525

gaa gac cag ccc ttc ccg gct gtg ccg aaa tgg tcc atc aaa aaa tgg    4029
Glu Asp Gln Pro Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys Trp
530                 535                 540                 545

ctt tcg cta cct gga gag acg cgc ccg ctg atc ctt tgc gaa tac gcc    4077
Leu Ser Leu Pro Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr Ala
                550                 555                 560

cac gcg atg ggt aac agt ctt ggc ggt ttc gct aaa tac tgg cag gcg    4125
His Ala Met Gly Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln Ala
            565                 570                 575

ttt cgt cag tat ccc cgt tta cag ggc ggc ttc gtc tgg gac tgg gtg    4173
Phe Arg Gln Tyr Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp Val
```

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                 580                      585                      590

gat cag tcg ctg att aaa tat gat gaa aac ggc aac ccg tgg tcg gct      4221
Asp Gln Ser Leu Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala
        595                      600                      605

tac ggc ggt gat ttt ggc gat acg ccg aac gat cgc cag ttc tgt atg      4269
Tyr Gly Gly Asp Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met
610                      615                      620                  625

aac ggt ctg gtc ttt gcc gac cgc acg ccg cat cca gcg ctg acg gaa      4317
Asn Gly Leu Val Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu
                630                      635                      640

gca aaa cac cag cag cag ttt ttc cag ttc cgt tta tcc ggg caa acc      4365
Ala Lys His Gln Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr
                645                      650                      655

atc gaa gtg acc agc gaa tac ctg ttc cgt cat agc gat aac gag ctc      4413
Ile Glu Val Thr Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu
                660                      665                      670

ctg cac tgg atg gtg gcg ctg gat ggt aag ccg ctg gca agc ggt gaa      4461
Leu His Trp Met Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu
        675                      680                      685

gtg cct ctg gat gtc gct cca caa ggt aaa cag ttg att gaa ctg cct      4509
Val Pro Leu Asp Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu Pro
690                      695                      700                  705

gaa cta ccg cag ccg gag agc gcc ggg caa ctc tgg ctc aca gta cgc      4557
Glu Leu Pro Gln Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val Arg
                710                      715                      720

gta gtg caa ccg aac gcg acc gca tgg tca gaa gcc ggg cac atc agc      4605
Val Val Gln Pro Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile Ser
                725                      730                      735

gcc tgg cag cag tgg cgt ctg gcg gaa aac ctc agt gtg acg ctc ccc      4653
Ala Trp Gln Gln Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu Pro
                740                      745                      750

gcc gcg tcc cac gcc atc ccg cat ctg acc acc agc gaa atg gat ttt      4701
Ala Ala Ser His Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp Phe
        755                      760                      765

tgc atc gag ctg ggt aat aag cgt tgg caa ttt aac cgc cag tca ggc      4749
Cys Ile Glu Leu Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser Gly
770                      775                      780                  785

ttt ctt tca cag atg tgg att ggc gat aaa aaa caa ctg ctg acg ccg      4797
Phe Leu Ser Gln Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr Pro
                790                      795                      800

ctg cgc gat cag ttc acc cgt gca ccg ctg gat aac gac att ggc gta      4845
Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly Val
                805                      810                      815

agt gaa gcg acc cgc att gac cct aac gcc tgg gtc gaa cgc tgg aag      4893
Ser Glu Ala Thr Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp Lys
        820                      825                      830
```

```
gcg gcg ggc cat tac cag gcc gaa gca gcg ttg ttg cag tgc acg gca      4941
Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr Ala
    835                 840                 845

gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg cag      4989
Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp Gln
850                 855                 860                 865

cat cag ggg aaa acc tta ttt atc agc cgg aaa acc tac cgg att gat      5037
His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile Asp
                870                 875                 880

ggt agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc gat      5085
Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser Asp
                885                 890                 895

aca ccg cat ccg gcg cgg att ggc ctg aac tgc cag ctg gcg cag gta      5133
Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln Val
        900                 905                 910

gca gag cgg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat ccc      5181
Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr Pro
    915                 920                 925

gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg tca      5229
Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu Ser
930                 935                 940                 945

gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc tgc      5277
Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg Cys
                950                 955                 960

ggg acg cgc gaa ttg aat tat ggc cca cac cag tgg cgc ggc gac ttc      5325
Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp Phe
                965                 970                 975

cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc agc      5373
Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser
            980                 985                 990

cat cgc cat ctg ctg cac gcg  gaa gaa ggc aca tgg  ctg aat atc gac   5421
His Arg His Leu Leu His Ala  Glu Glu Gly Thr Trp  Leu Asn Ile Asp
    995                 1000                1005

ggt  ttc cat atg ggg att  ggt ggc gac gac tcc  tgg agc ccg tca      5466
Gly  Phe His Met Gly Ile  Gly Gly Asp Asp Ser  Trp Ser Pro Ser
1010                1015                1020

gta tcg gcg gaa ttc cag  ctg agc gcc ggt cgc  tac cat tac cag      5511
Val Ser Ala Glu Phe Gln  Leu Ser Ala Gly Arg  Tyr His Tyr Gln
1025                1030                1035

ttg gtc tgg tgt caa aaa  taa tgactgcagg tcgaccatag tgactggata      5562
Leu Val Trp Cys Gln Lys
1040                1045

tgttgtgttt tacagtatta tgtagtctgt tttttatgca aaatctaatt taatatattg   5622

atatttatat cattttacgt ttctcgttca gctttcttgt acaaagtggt gagaatgaat   5682
```

```
gaagatctg ggg aag cct atc cct   aac cct ctc ctc ggt   ctc gat tct         5730
          Gly Lys Pro Ile Pro   Asn Pro Leu Leu Gly   Leu Asp Ser
                       1050                   1055

acg cgt  acc ggt cat cat cac   cat cac cat tga                            5763
Thr Arg  Thr Gly His His His   His His His
    1060              1065
```

<210> 95
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Mel/V5-His DEST cassette

<400> 95

```
Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1               5                  10                  15


Ser Tyr Ile Tyr Ala
            20
```

<210> 96
<211> 1024
<212> PRT
<213> Artificial Sequence

<220>
<223> Mel/V5-His DEST cassette

<400> 96

```
Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Arg Asp
1               5                  10                  15


Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
            20                  25                  30


Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro
        35                  40                  45


Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe
    50                  55                  60


Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu Glu Cys Asp Leu Pro
65                  70                  75                  80


Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
                85                  90                  95
```

Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro
          100   105   110

Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys Tyr Ser Leu Thr Phe
          115   120   125

Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln Thr Arg Ile Ile Phe
          130   135   140

Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn Gly Arg Trp Val
145   150   155   160

Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu Phe Asp Leu Ser Ala
                165   170   175

Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val Met Val Leu Arg Trp
          180   185   190

Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp Arg Met Ser Gly
          195   200   205

Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro Thr Thr Gln Ile Ser
          210   215   220

Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp Phe Ser Arg Ala Val
225   230   235   240

Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu Arg Asp Tyr Leu Arg
                245   250   255

Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln Val Ala Ser Gly Thr
              260   265   270

Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg Gly Gly Tyr Ala Asp
          275   280   285

Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro Lys Leu Trp Ser Ala
          290   295   300

Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu Leu His Thr Ala Asp
305   310   315   320

Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val Gly Phe Arg Glu Val
              325   330   335

Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly Lys Pro Leu Leu Ile

```
                340                      345                      350

Arg Gly Val Asn Arg His Glu His His Pro Leu His Gly Gln Val Met
        355                 360                 365

Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu Met Lys Gln Asn Asn
        370                 375                 380

Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn His Pro Leu Trp Tyr
385                      390                 395                 400

Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val Asp Glu Ala Asn Ile
                405                 410                 415

Glu Thr His Gly Met Val Pro Met Asn Arg Leu Thr Asp Asp Pro Arg
            420                 425                 430

Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg Met Val Gln Arg Asp
            435                 440                 445

Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu Gly Asn Glu Ser Gly
    450                 455                 460

His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp Ile Lys Ser Val Asp
465                 470                 475                 480

Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly Ala Asp Thr Thr Ala
                485                 490                 495

Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro
            500                 505                 510

Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys Trp Leu Ser Leu Pro
            515                 520                 525

Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly
        530                 535                 540

Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln Ala Phe Arg Gln Tyr
545                 550                 555                 560

Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp Val Asp Gln Ser Leu
                565                 570                 575

Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala Tyr Gly Gly Asp
            580                 585                 590
```

Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met Asn Gly Leu Val
    595   600   605

Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu Ala Lys His Gln
    610   615   620

Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr Ile Glu Val Thr
625   630   635   640

Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Met
         645   650   655

Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu Val Pro Leu Asp
        660   665   670

Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu Pro Glu Leu Pro Gln
        675   680   685

Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val Arg Val Val Gln Pro
    690   695   700

Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile Ser Ala Trp Gln Gln
705   710   715   720

Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu Pro Ala Ala Ser His
        725   730   735

Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp Phe Cys Ile Glu Leu
        740   745   750

Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser Gly Phe Leu Ser Gln
        755   760   765

Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr Pro Leu Arg Asp Gln
    770   775   780

Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly Val Ser Glu Ala Thr
785   790   795   800

Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp Lys Ala Ala Gly His
        805   810   815

Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr Ala Asp Thr Leu Ala
        820   825   830

Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp Gln His Gln Gly Lys
   835   840   845

Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile Asp Gly Ser Gly Gln
   850   855   860

Met Ala Ile Thr Val Asp Val Glu Val Ala Ser Asp Thr Pro His Pro
865   870   875   880

Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln Val Ala Glu Arg Val
      885   890   895

Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr Pro Asp Arg Leu Thr
     900   905   910

Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu Ser Asp Met Tyr Thr
    915   920   925

Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg Cys Gly Thr Arg Glu
   930   935   940

Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp Phe Gln Phe Asn Ile
945   950   955   960

Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser His Arg His Leu
     965   970   975

Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile Asp Gly Phe His Met
    980   985   990

Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser Val Ser Ala Glu Phe
    995   1000   1005

Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu Val Trp Cys Gln
  1010   1015   1020

Lys

<210> 97
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Mel/V5-His DEST cassette

<400> 97

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Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
1               5                   10                  15
```

```
Gly His His His His His
            20
```

```
<210>  98
<211>  1021
<212>  DNA
<213>  Unknown
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```
<220>
<223>  AcMNPV ORF 25   promoter sequence
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<400>  98
ggtgtcttca ttagtatgcc aatcacgtac gcaacagtcg caaaagaaac acacagtttc    60

gtctccgcga cccgtgtaaa aaagtcccgc ttccgcaatg tttgtaatca tgtcacgcaa   120

tgcggcaggc caaaagttaa caaacgtatc catacgcgac tgtaaattgg acatgcatct   180

gtacacacac ttgggtttgc cttctttcac tagtacagcg ttgatggtaa tgttgtcgcc   240

aaacgattca cgctcggcga tcttgttagc atacgcgcaa tacggcgaca aggttacgtg   300

tgcatattca atacactcgt cttcggacca attttttatt tctgcttcgc aatactcgca   360

cacaacgtga tcgtcaactt gattgtattt aaacccgtta acgatcaagc tgttaataaa   420

cgccgtgttt tcaatgggat aattttcaaa cgaactatgt ctttctatta acatgtcgaa   480

tacgtgttcg gcggtgttgt cgcgaaagtt gtcacacacg ctgataaaat aaaacggggg   540

cgtgtcctcg ttcattttag ctcgttaaag ttacggtcaa aatgagcacg tttgcgtcgt   600

tttggtttag cgacacgttt atatggccca gtttggtttt tgtttcggcg ttaatgacgt   660

gcactgtgga caaatcgtgt tctaaaacta caaactcgta ctcgaaaatg tttgatatgt   720

agttggttag ccgatctatc ttaaaattaa acttttgcaa ctcgctgata gagcacacgt   780

ccacatactt gtcgataaac ccgttgctca accgcttcaa aacggtgtaa ttttgtagct   840

tgaaaggggc gcatttggaa tgactaaaag gaatattttt caataaatcg tcagtagtgt   900

acgcaaacgc gttgtctacg cacatgctgg caacagagtc gtccatattt attatatatc   960

ttatattctg tgaaacactt caattagact tgaaccacag cagacagcgc acgtcggtag  1020

c                                                                   1021
```

```
<210>  99
<211>  1033
<212>  DNA
<213>  Unknown
```

```
<220>
<223>  AcMNPV lef 3 promoter

<400>  99
ccgagaagaa ggcggtttgt ataaaaccca tttttcgaaa tggttaacaa acttgtttag      60

catttggatc gtttcgtgtt caaacgcgtc gaaaacttt  aaaacgcaat tgccgccggg     120

acgcaggcaa attaaaatta gctgcgtctc gcacatgatc aaatcaaagt tgagacgttc     180

ttgttcgttt tcgcgtccat taacgtcaac cgagccatct gccaacacca gatcgcacgc     240

gttgccacac ttgatgctaa tctcaaatac aacatttta  tcaaacacgt cgcctgactt     300

gtcgggcccc gtaatggttg tgaaatttt  gcgtttgcgc actgtcggtt tgtacacgca     360

caccgagttg tttgtcaacg tgacgccata cgctttgcaa agcgggttca acgacatggt     420

atagttggca aactcgcccg gtccgccgca caaatccaaa aacgtgtcaa cgtgtcggca     480

aacgtgaaac tttttgtcga tctctgatag ttttcgccaa catctaggtc tgcgcgttgg     540

gcgtttgtca ataatttttg agcgagcgca aaccaccgac ttgctgctga acgtgttcaa     600

accatctttg agtttattta atttttgctg caacatttt  actcttcgtg tcggtcgcaa     660

tgtttgtgtc gaaaaagacg gccaacacgc tcagcaaaac tatacaaata aagaacaaaa     720

atacgtacgc aatattaaca ttgaccgttt gatcgttaaa tcggacgggt ctgttcagag     780

ccgctcttat tctctcgttg tacattgtta aagtttttgt ttttaaattg tacacaatcg     840

gcgtgttgta gtcgaaattt tcaaaatcgg cttttgaaa  cattgttctg aacgtgttgt     900

cgagcggcgt gttgctggcc acgtttataa tcaactccct ccacgctaac gaacggtgct     960

ctggcgacac ttcgatttcg tcgccattca gtatttgcca tcggatagat tcccacatat    1020

cgacaacagc aat                                                       1033


<210>  100
<211>  1053
<212>  DNA
<213>  Unknown

<220>
<223>  AcMNPV TLP promoter

<400>  100
tgctagccca attggccact gttgtacgaa atatcgtcgt caacgtgttt gaatacatgt      60

tggcccgtac cgttgggtaa atctatgcat ctggagtcgc cggaacactc gtactggttg     120

tcagagtttc tgatccggtt gatgcacgtt atcagttgtg actcgttatt attcaaacat     180

ttgaaatatt gcgtgtcgcc gatatcggcc gttatgtacg tgtgtccggc gccgttaaac     240

gcgcacggat gcgcttccac gcacgacatt aagttgcgat caaatatttt attcgcgggg     300

cattcgccca ccacgtggcg cccatttacg cactgcataa actggttgac gagcaaattg     360
```

```
gagggaaagt atgatagtat atagccgtct ggcctgtttt cacacaattc gttaacttta      420

cactggccgg tttccgcgtc aaacgtgtaa ttatctggac attcttcgac tgcgtgcgct      480

ccgtttgcaa aacacctaag atagaacgtg ggatgataca agtgcgcgtt ggtagaataa      540

tctttgtcca agtgttggtt caacaccaac gtgtccagca aacgctcgtc catgggataa      600

agaccggcag acttgttgtc gcacggcggc acgggaacac attttagttg tgcgtaatca      660

aagttaaaat atgcggggca tttcatggtc acgtcggcct tgtcgccgct caaaataaac      720

tcgttgggat tttcatcatt tgctctaacg cgatcgtgta cgattcgatc aacaggttga      780

aatttttgat ttaagaaatc aaaaatttca atccggtcat catgcacgct ttcgtgatag      840

gtggaaaggt cgacggtgtt gaaccacgtt acaatataag tgttttgcat aatatccgac      900

acgtagccta ttacgtcggg tgtgggttcg tctgcgttgg tgcgcttcac atattcagtc      960

atcacttgga gccgcttggt gaaagtcgtt tcgtcaaatt caaaataaat tgccaaatac     1020

attaaagtaa acgctattat aagaaaaaag ctt                                  1053
```

<210> 101
<211> 507
<212> DNA
<213> Unknown

<220>
<223> AcMNPV hr5 sequence

<400> 101
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gttttacgcg tagaattcta cccgtaaagc gagtttagtt atgagccatg tgcaaaacat       60

gacatcagct tttattttta taacaaatga catcatttct tgattgtgtt ttacacgtag      120

aattctactc gtaaagcgag ttcagttttg aaaaacaaat gacatcatct ttttgattgt      180

gctttacaag tagaattcta cccgtaaatc aagttcggtt ttgaaaaaca aatgagtcat      240

attgtatgat atcatattgc aaacaaatga ctcatcaatc gatcgtgcgt acacgtagaa      300

ttctactcgt aaagcgagtt tatgagccgt gtgcaaaaca tgacatcatc tcgatttgaa      360

aaacaaatga catcatccac tgatcgtgcg ttacaagtag aattctactc gtaaagccag      420

ttcggttatg agccgtgtgc aaaacatgac atcagcttat gactcgtact tgattgtgtt      480

ttacgcgtag aattctactc gtaaagc                                         507
```

<210> 102
<211> 507
<212> DNA
<213> Unknown

<220>
<223> AcMNPV IE-1 promoter

<400> 102

```
gttttacgcg tagaattcta cccgtaaagc gagtttagtt atgagccatg tgcaaaacat      60

gacatcagct tttatttta taacaaatga catcatttct tgattgtgtt ttacacgtag     120

aattctactc gtaaagcgag ttcagttttg aaaaacaaat gacatcatct ttttgattgt     180

gctttacaag tagaattcta cccgtaaatc aagttcggtt ttgaaaaaca aatgagtcat     240

attgtatgat atcatattgc aaacaaatga ctcatcaatc gatcgtgcgt acacgtagaa     300

ttctactcgt aaagcgagtt tatgagccgt gtgcaaaaca tgacatcatc tcgatttgaa     360

aaacaaatga catcatccac tgatcgtgcg ttacaagtag aattctactc gtaaagccag     420

ttcggttatg agccgtgtgc aaaacatgac atcagcttat gactcgtact tgattgtgtt     480

ttacgcgtag aattctactc gtaaagc                                        507
```

<210> 103
<211> 1746
<212> DNA
<213> Unknown

<220>
<223> AcMPNV IE-1 coding sequence

<400> 103

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atgacgcaaa ttaatttaa cgcgtcgtac accagcgctt cgacgccgtc ccgagcgtcg      60

ttcgacaaca gctattcaga gttttgtgat aaacaaccca acgactattt aagttattat     120

aaccatccca ccccggatgg agccgacacg gtgatatctg acagcgagac tgcggcagct     180

tcaaactttt tggcaagcgt caactcgtta actgataatg atttagtgga atgtttgctc     240

aagaccactg ataatctcga agaagcagtt agttctgctt attattcgga atcccttgag     300

cagcctgttg tggagcaacc atcgcccagt tctgcttatc atgcggaatc ttttgagcat     360

tctgctggtg tgaaccaacc atcggcaact ggaactaaac ggaagctgga cgaatacttg     420

gacaattcac aaggtgtggt gggccagttt aacaaaatta aattgaggcc taaatacaag     480

aaaagcacaa ttcaaagctg tgcaacccctt gaacagacaa ttaatcacaa cacgaacatt     540

tgcacggtcg cttcaactca agaaattacg cattattta ctaatgattt tgcgccgtat     600

ttaatgcgtt tcgacgacaa cgactacaat ccaacaggt tctccgacca tatgtccgaa     660

actggttatt acatgtttgt ggttaaaaaa agtgaagtga gccgtttga aattatattt     720

gccaagtacg tgagcaatgt ggtttacgaa tatacaaaca attattacat ggtagataat     780

cgcgtgtttg tggtaacttt tgataaaatt aggtttatga tttcgtacaa tttggttaaa     840

gaaaccggca tagaaattcc tcattctcaa gatgtgtgca acgacgagac ggctgcacaa     900

aattgtaaaa aatgccattt cgtcgatgtg caccacacgt ttaaagctgc tctgacttca     960
```

tattttaatt tagatatgta ttacgcgcaa accacatttg tgactttgtt acaatcgttg   1020

ggcgaaagaa aatgtgggtt tcttttgagc aagttgtacg aaatgtatca agataaaaat   1080

ttatttactt tgcctattat gcttagtcgt aaagagagta atgaaattga gactgcatct   1140

aataatttct ttgtatcgcc gtatgtgagt caaatattaa agtattcgga aagtgtgcag   1200

tttcccgaca atcccccaaa caaatatgtg gtggacaatt taaatttaat tgttaacaaa   1260

aaaagtacgc tcacgtacaa atacagcagc gtcgctaatc ttttgtttaa taattataaa   1320

tatcatgaca atattgcgag taataataac gcagaaaatt taaaaaaggt taagaaggag   1380

gacggcagca tgcacattgt cgaacagtat ttgactcaga atgtagataa tgtaaagggt   1440

cacaatttta tagtattgtc tttcaaaaac gaggagcgat tgactatagc taagaaaaac   1500

aaagagtttt attggatttc tggcgaaatt aaagatgtag acgttagtca agtaattcaa   1560

aaatataata gatttaagca tcacatgttt gtaatcggta aagtgaaccg aagagagagc   1620

actacattgc acaataattt gttaaaattg ttagctttaa tattacaggg tctggttccg   1680

ttgtccgacg ctataacgtt tgcggaacaa aaactaaatt gtaaatataa aaaattcgaa   1740

tttaat   1746

<210>   104
<211>   582
<212>   PRT
<213>   Unknown

<220>
<223>   AcMNPV IE-1 protein sequence

<400>   104

Met Thr Gln Ile Asn Phe Asn Ala Ser Tyr Thr Ser Ala Ser Thr Pro
1   5   10   15

Ser Arg Ala Ser Phe Asp Asn Ser Tyr Ser Glu Phe Cys Asp Lys Gln
            20   25   30

Pro Asn Asp Tyr Leu Ser Tyr Tyr Asn His Pro Thr Pro Asp Gly Ala
        35   40   45

Asp Thr Val Ile Ser Asp Ser Glu Thr Ala Ala Ala Ser Asn Phe Leu
    50   55   60

Ala Ser Val Asn Ser Leu Thr Asp Asn Asp Leu Val Glu Cys Leu Leu
65   70   75   80

Lys Thr Thr Asp Asn Leu Glu Glu Ala Val Ser Ser Ala Tyr Tyr Ser

                    85   90   95

Glu Ser Leu Glu Gln Pro Val Val Glu Gln Pro Ser Pro Ser Ser Ala
            100   105   ʹ   110

Tyr His Ala Glu Ser Phe Glu His Ser Ala Gly Val Asn Gln Pro Ser
            115   120   125

Ala Thr Gly Thr Lys Arg Lys Leu Asp Glu Tyr Leu Asp Asn Ser Gln
    130   135   140

Gly Val Val Gly Gln Phe Asn Lys Ile Lys Leu Arg Pro Lys Tyr Lys
145   150   155   160

Lys Ser Thr Ile Gln Ser Cys Ala Thr Leu Glu Gln Thr Ile Asn His
                165   170   175

Asn Thr Asn Ile Cys Thr Val Ala Ser Thr Gln Glu Ile Thr His Tyr
            180   185   190

Phe Thr Asn Asp Phe Ala Pro Tyr Leu Met Arg Phe Asp Asp Asn Asp
            195   200   205

Tyr Asn Ser Asn Arg Phe Ser Asp His Met Ser Glu Thr Gly Tyr Tyr
    210   215   220

Met Phe Val Val Lys Lys Ser Glu Val Lys Pro Phe Glu Ile Ile Phe
225   230   235   240

Ala Lys Tyr Val Ser Asn Val Val Tyr Glu Tyr Thr Asn Asn Tyr Tyr
            245   250   255

Met Val Asp Asn Arg Val Phe Val Val Thr Phe Asp Lys Ile Arg Phe
            260   265   270

Met Ile Ser Tyr Asn Leu Val Lys Glu Thr Gly Ile Glu Ile Pro His
            275   280   285

Ser Gln Asp Val Cys Asn Asp Glu Thr Ala Ala Gln Asn Cys Lys Lys
    290   295   300

Cys His Phe Val Asp Val His His Thr Phe Lys Ala Ala Leu Thr Ser
305   310   315   320

Tyr Phe Asn Leu Asp Met Tyr Tyr Ala Gln Thr Thr Phe Val Thr Leu
            325   330   335

Leu Gln Ser Leu Gly Glu Arg Lys Cys Gly Phe Leu Leu Ser Lys Leu
        340   345   350

Tyr Glu Met Tyr Gln Asp Lys Asn Leu Phe Thr Leu Pro Ile Met Leu
        355   360   365

Ser Arg Lys Glu Ser Asn Glu Ile Glu Thr Ala Ser Asn Asn Phe Phe
        370   375   380

Val Ser Pro Tyr Val Ser Gln Ile Leu Lys Tyr Ser Glu Ser Val Gln
385   390   395   400

Phe Pro Asp Asn Pro Pro Asn Lys Tyr Val Val Asp Asn Leu Asn Leu
                405   410   415

Ile Val Asn Lys Lys Ser Thr Leu Thr Tyr Lys Tyr Ser Ser Val Ala
                420   425   430

Asn Leu Leu Phe Asn Asn Tyr Lys Tyr His Asp Asn Ile Ala Ser Asn
        435   440   445

Asn Asn Ala Glu Asn Leu Lys Lys Val Lys Lys Glu Asp Gly Ser Met
        450   455   460

His Ile Val Glu Gln Tyr Leu Thr Gln Asn Val Asp Asn Val Lys Gly
465   470   475   480

His Asn Phe Ile Val Leu Ser Phe Lys Asn Glu Glu Arg Leu Thr Ile
                485   490   495

Ala Lys Lys Asn Lys Glu Phe Tyr Trp Ile Ser Gly Glu Ile Lys Asp
                500   505   510

Val Asp Val Ser Gln Val Ile Gln Lys Tyr Asn Arg Phe Lys His His
                515   520   525

Met Phe Val Ile Gly Lys Val Asn Arg Arg Glu Ser Thr Thr Leu His
        530   535   540

Asn Asn Leu Leu Lys Leu Leu Ala Leu Ile Leu Gln Gly Leu Val Pro
545   550   555   560

Leu Ser Asp Ala Ile Thr Phe Ala Glu Gln Lys Leu Asn Cys Lys Tyr
                565   570   575

```
Lys Lys Phe Glu Phe Asn
            580


<210>   105
<211>   8688
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   pLenti6/V5-DEST

<400>   105
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tgccttacaa ggagagaaaa agcaccgtgc atgccgattg gtggaagtaa ggtggtacga     120

tcgtgcctta ttaggaaggc aacagacggg tctgacatgg attggacgaa ccactgaatt     180

gccgcattgc agagatattg tatttaagtg cctagctcga tacataaacg ggtctctctg     240

gttagaccag atctgagcct gggagctctc tggctaacta gggaacccac tgcttaagcc     300

tcaataaagc ttgccttgag tgcttcaagt agtgtgtgcc cgtctgttgt gtgactctgg     360

taactagaga tccctcagac cctttttagtc agtgtggaaa atctctagca gtggcgcccg     420

aacagggact tgaaagcgaa agggaaacca gaggagctct ctcgacgcag gactcggctt     480

gctgaagcgc gcacggcaag aggcgagggg cggcgactgg tgagtacgcc aaaaattttg     540

actagcggag gctagaagga gagagatggg tgcgagagcg tcagtattaa gcggggggaga     600

attagatcgc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta     660

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta     720

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga     780

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg     840

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt     900

aagaccaccg cacagcaagc ggccgctgat cttcagacct ggaggaggag atatgaggga     960

caattggaga agtgaattat ataaatataa agtagtaaaa attgaaccat taggagtagc    1020

acccaccaag gcaaagagaa gagtggtgca gagagaaaaa agagcagtgg aataggagc     1080

tttgttcctt gggttcttgg gagcagcagg aagcactatg ggcgcagcgt caatgacgct    1140

gacggtacag gccagacaat tattgtctgg tatagtgcag cagcagaaca atttgctgag    1200

ggctattgag gcgcaacagc atctgttgca actcacagtc tggggcatca agcagctcca    1260

ggcaagaatc ctggctgtgg aaagatacct aaaggatcaa cagctcctgg gatttgggg    1320

ttgctctgga aaactcattt gcaccactgc tgtgccttgg aatgctagtt ggagtaataa    1380

atctctggaa cagatttgga atcacacgac ctggatggag tgggacagag aaattaacaa    1440
```

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ttacacaagc ttaatacact ccttaattga agaatcgcaa aaccagcaag aaaagaatga   1500

acaagaatta ttggaattag ataaatgggc aagtttgtgg aattggttta acataacaaa   1560

ttggctgtgg tatataaaat tattcataat gatagtagga ggcttggtag gtttaagaat   1620

agtttttgct gtactttcta tagtgaatag agttaggcag ggatattcac cattatcgtt   1680

tcagacccac ctcccaaccc cgaggggacc cgacaggccc gaaggaatag aagaagaagg   1740

tggagagaga gacagagaca gatccattcg attagtgaac ggatctcgac ggtatcgata   1800

agcttgggag ttccgcgtta cataacttac ggtaaatggc ccgcctggct gaccgcccaa   1860

cgacccccgc ccattgacgt caataatgac gtatgttccc atagtaacgc caatagggac   1920

tttccattga cgtcaatggg tggagtattt acggtaaact gcccacttgg cagtacatca   1980

agtgtatcat atgccaagta cgccccctat tgacgtcaat gacggtaaat ggcccgcctg   2040

gcattatgcc cagtacatga ccttatggga ctttcctact tggcagtaca tctacgtatt   2100

agtcatcgct attaccatgg tgatgcggtt ttggcagtac atcaatgggc gtggatagcg   2160

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gctacacttg  ccagcgccct  agcgcccgct  cctttcgctt  tcttcccttc  ctttctcgcc  4500

acgttcgccg  gctttccccg  tcaagctcta  aatcggggc   tccctttagg  gttccgattt  4560

agtgctttac  ggcacctcga  ccccaaaaaa  cttgattagg  gtgatggttc  acgtagtggg  4620

ccatcgccct  gatagacggt  ttttcgccct  ttgacgttgg  agtccacgtt  ctttaatagt  4680

ggactcttgt  tccaaactgg  aacaacactc  aaccctatct  cggtctattc  ttttgattta  4740

taagggattt  tgccgatttc  ggcctattgg  ttaaaaaatg  agctgattta  acaaaaattt  4800

aacgcgaatt  ttaacaaaat  attaacgttt  acaatttccc  aggtggcact  tttcggggaa  4860

atgtgcgcgg  aacccctatt  tgtttatttt  tctaaataca  ttcaaatatg  tatccgctca  4920

tgagacaata  accctgataa  atgcttcaat  aatattgaaa  aaggaagagt  atgagtattc  4980

aacatttccg  tgtcgccctt  attcccttt   ttgcggcatt  ttgccttcct  gtttttgctc  5040

acccagaaac  gctggtgaaa  gtaaagatg   ctgaagatca  gttgggtgca  cgagtgggtt  5100

acatcgaact  ggatctcaac  agcggtaaga  tccttgagag  ttttcgcccc  gaagaacgtt  5160

ttccaatgat  gagcactttt  aaagttctgc  tatgtggcgc  ggtattatcc  cgtattgacg  5220

ccgggcaaga  gcaactcggt  cgccgcatac  actattctca  gaatgacttg  gttgagtact  5280

caccagtcac  agaaaagcat  cttacggatg  gcatgacagt  aagagaatta  tgcagtgctg  5340
```

```
ccataaccat gagtgataac actgcggcca acttacttct gacaacgatc ggaggaccga      5400

aggagctaac cgctttttttg cacaacatgg gggatcatgt aactcgcctt gatcgttggg      5460

aaccggagct gaatgaagcc ataccaaacg acgagcgtga caccacgatg cctgtagcaa      5520

tggcaacaac gttgcgcaaa ctattaactg gcgaactact tactctagct tcccggcaac      5580

aattaataga ctggatggag gcggataaag ttgcaggacc acttctgcgc tcggcccttc      5640

cggctggctg gtttattgct gataaatctg gagccggtga gcgtgggtct cgcggtatca      5700

ttgcagcact ggggccagat ggtaagccct cccgtatcgt agttatctac acgacgggga      5760

gtcaggcaac tatggatgaa cgaaatagac agatcgctga gataggtgcc tcactgatta      5820

agcattggta actgtcagac caagtttact catatatact ttagattgat ttaaaacttc      5880

atttttaatt taaaaggatc taggtgaaga tcctttttga taatctcatg accaaaatcc      5940

cttaacgtga gttttcgttc cactgagcgt cagaccccgt agaaaagatc aaaggatctt      6000

cttgagatcc ttttttttctg cgcgtaatct gctgcttgca acaaaaaaa ccaccgctac      6060

cagcggtggt ttgtttgccg gatcaagagc taccaactct ttttccgaag gtaactggct      6120

tcagcagagc gcagatacca aatactgtcc ttctagtgta gccgtagtta ggccaccact      6180

tcaagaactc tgtagcaccg cctacatacc tcgctctgct aatcctgtta ccagtggctg      6240

ctgccagtgg cgataagtcg tgtcttaccg ggttggactc aagacgatag ttaccggata      6300

aggcgcagcg tcgggctga acggggggtt cgtgcacaca gcccagcttg gagcgaacga      6360

cctacaccga actgagatac ctacagcgtg agctatgaga aagcgccacg cttcccgaag      6420

ggagaaaggc ggacaggtat ccggtaagcg gcagggtcgg aacaggagag cgcacgaggg      6480

agcttccagg gggaaacgcc tggtatcttt atagtcctgt cgggtttcgc cacctctgac      6540

ttgagcgtcg atttttgtga tgctcgtcag ggggggcggag cctatggaaa aacgccagca      6600

acgcggcctt tttacggttc ctggcctttt gctggccttt tgctcacatg ttctttcctg      6660

cgttatcccc tgattctgtg ataaccgta ttaccgcctt tgagtgagct gataccgctc      6720

gccgcagccg aacgaccgag cgcagcgagt cagtgagcga ggaagcggaa gagcgcccaa      6780

tacgcaaacc gcctctcccc gcgcgttggc cgattcatta atgcagctgg cacgacaggt      6840

ttcccgactg gaaagcgggc agtgagcgca acgcaattaa tgtgagttag ctcactcatt      6900

aggcacccca ggctttacac tttatgcttc cggctcgtat gttgtgtgga attgtgagcg      6960

gataacaatt tcacacagga aacagctatg accatgatta cgccaagcgc gcaattaacc      7020

ctcactaaag ggaacaaaag ctggagctgc aagctt                               7056
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<210> 121

<211> 172
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pAd/CMV/V5-DEST

<220>
<221> misc_feature
<222> (172)..(172)
<223> n may be any nucleotide

<400> 121
ttgacgcaaa tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctctctgg   60

ctaactagag aacccactgc ttactggctt atcgaaatta atacgactca ctatagggag   120

acccaagctg gctagttaag ctatcaacaa gtttgtacaa aaaagcaggc tn   172

<210> 122
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pAd/CMV/V5-DEST

<220>
<221> misc_feature
<222> (1)..(1)
<223> n may be any nucleotide

<220>
<221> CDS
<222> (4)..(105)

<400> 122
nac cca gct ttc ttg tac aaa gtg gtt gat cta gag ggc ccg cgg ttc   48
    Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe
    1   5   10   15

gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt   96
Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg
                20   25   30

acc ggt tag taatgagttt aaacggggga ggctaactga   135
Thr Gly

<210> 123
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombination region of pAd/CMV/V5-DEST

<400> 123

Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe Glu
1   5   10   15

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
            20   25   30

Gly

<210>   124
<211>   197
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Recombination region of pAd/PL-DEST

<220>
<221>   misc_feature
<222>   (197)..(197)
<223>   n may be any nucleotide

<400>   124
tatttgtcta gggccgcggg gactttgacc gtttacgtgg agactcgccc aggtgttttt   60

ctcaggtgtt ttccgcgttc cgggtcaaag ttggcgtttt attattatag tcagtcgaag   120

cttggatccg gtacctctag aattctcgag cggccgctag cgacatcgat cacaagtttg   180

tacaaaaaag caggctn   197

<210>   125
<211>   90
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Recombination region of pAd/PL-DEST

<220>
<221>   misc_feature
<222>   (1)..(1)
<223>   n may be any nucleotide

<400>   125
nacccagctt tcttgtacaa agtggtgatc gattcgacag atcactgaaa tgtgtgggcg   60

tggcttaagg gtgggaaaga atatataagg   90

<210>   126
<211>   560
<212>   DNA

<213> Unknown

<220>
<223> OpIE2 promoter sequence

<400> 126
ggatcatgat gataaacaat gtatggtgct aatgttgctt caacaacaat tctgttgaac   60

tgtgttttca tgtttgccaa caagcacctt tatactcggt ggcctcccca ccaccaactt   120

ttttgcactg caaaaaaaca cgcttttgca cgcgggccca tacatagtac aaactctacg   180

tttcgtagac tattttacat aaatagtcta caccgttgta tacgctccaa atacactacc   240

acacattgaa cctttttgca gtgcaaaaaa gtacgtgtcg gcagtcacgt aggccggcct   300

tatcgggtcg cgtcctgtca cgtacgaatc acattatcgg accggacgag tgttgtctta   360

tcgtgacagg acgccagctt cctgtgttgc taaccgcagc cggacgcaac tccttatcgg   420

aacaggacgc gcctccatat cagccgcgcg ttatctcatg cgcgtgaccg gacacgaggc   480

gcccgtcccg cttatcgcgc ctataaatac agcccgcaac gatctggtaa acacagttga   540

acagcatctg ttcgaattta   560

<210> 127
<211> 147
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pIB/V5-His-DEST

<220>
<221> misc_feature
<222> (141)..(148)
<223> n may be any nucleotide

<400> 127
cttatcgcgc ctataaatac agcccgcaac gatctggtaa acacagttga acagcatctg   60

ttcgaattta aagcttgata tcgaattcct gcagcccagc gctggatcct cgatcacaag   120

tttgtacaaa aaagcaggct nnnnnnn   147

<210> 128
<211> 184
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pIB/V5-His-DEST

<220>
<221> misc_feature
<222> (1)..(1)

<223>   n may be any nucleotide

<220>
<221>   CDS
<222>   (4)..(135)

<400>   128
nac cca cca gct ttc ttg tac aaa gtg gtg atc gac ccg ggt cta gag   48
    Pro Pro Ala Phe Leu Tyr Lys Val Val Ile Asp Pro Gly Leu Glu
    1   5   10   15

ggc ccg cgg ttc gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc   96
Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu
                20   25   30

gat tct acg cgt acc ggt cat cat cac cat cac cat tga gtttatctga   145
Asp Ser Thr Arg Thr Gly His His His His His His
            35   40

ctaaatctta gttgtattgt catgttttaa tacaatatg   184

<210>   129
<211>   43
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Recombination region of pIB/V5-His-DEST

<400>   129

Pro Pro Ala Phe Leu Tyr Lys Val Val Ile Asp Pro Gly Leu Glu Gly
1   5   10   15

Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp
                20   25   30

Ser Thr Arg Thr Gly His His His His His His
        35   40

<210>   130
<211>   215
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Recombination region of pLenti6/V5-DEST

<220>
<221>   misc_feature
<222>   (215)..(215)
<223>   n may be any nucleotide

<400>   130
tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta   60

```
tataagcaga gctcgtttag tgaaccgtca gatcgcctgg agacgccatc cacgctgttt    120

tgacctccat agaagacacc gactctagag gatccactag tccagtgtgg tggaattctg    180

cagatatcaa caagtttgta caaaaaagca ggctn                               215
```

```
<210>  131
<211>  142
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Recombination region of pLenti6/V5-DEST


<220>
<221>  misc_feature
<222>  (1)..(1)
<223>  n may be any nucleotide

<220>
<221>  CDS
<222>  (4)..(132)

<400>  131
nac cca gct ttc ttg tac aaa gtg gtt gat atc cag cac agt ggc ggc    48
    Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly
    1               5                   10                  15

cgc tcg agt cta gag ggc ccg cgg ttc gaa ggt aag cct atc cct aac    96
Arg Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn
            20                  25                  30

cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag taatgagttt        142
Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
            35                  40
```

```
<210>  132
<211>  42
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Recombination region of pLenti6/V5-DEST

<400>  132

Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly Arg
1               5                   10                  15


Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro
            20                  25                  30


Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
            35                  40
```

<210> 133
<211> 217
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of the expression clone resulting from
pLenti6/UbC/V5-DEST x entry clone

<220>
<221> misc_feature
<222> (217)..(217)
<223> n may be any nucleotide

<400> 133
ttggcgagtg tgttttgtga agttttttag gcacctttg aaatgtaatc atttgggtca   60

atatgtaatt ttcagtgtta gactagtaaa ttgtccgcta aattctggcc gtttttggct   120

tttttgttag acgaagcttg gtaccgagct cggatccact agtccagtgt ggtggaattc   180

tgcagatatc aacaagtttg tacaaaaaag caggctn   217

<210> 134
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of the expression clone resulting from
pLenti6/UbC/V5-DEST x entry clone

<220>
<221> misc_feature
<222> (1)..(1)
<223> n may be any nucleotide

<220>
<221> CDS
<222> (4)..(132)

<400> 134
nac cca gct ttc ttg tac aaa gtg gtt gat atc cag cac agt ggc ggc   48
    Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly
    1   5   10   15

cgc tcg agt cta gag ggc ccg cgg ttc gaa ggt aag cct atc cct aac   96
Arg Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn
                20   25   30

cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag taatgagttt   142
Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
                35   40

<210> 135
<211> 42
<212> PRT

<213>   Artificial Sequence

<220>
<223>   Recombination region of the expression clone resulting from
       pLenti6/UbC/V5-DEST x entry clone

<400>   135

Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly Arg
1   5   10   15

Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro
            20   25   30

Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
        35   40

<210>   136
<211>   1226
<212>   DNA
<213>   Unknown

<220>
<223>   Sequence of the UbC promoter

<400>   136
cggatctggc ctccgcgccg ggtttttggcg cctcccgcgg gcgcccccct cctcacggcg   60

agcgctgcca cgtcagacga agggcgcagg agcgtcctga tccttccgcc cggacgctca   120

ggacagcggc ccgctgctca taagactcgg ccttagaacc ccagtatcag cagaaggaca   180

ttttaggacg ggacttgggt gactctaggg cactggtttt ctttccagag agcggaacag   240

gcgaggaaaa gtagtccctt ctcggcgatt ctgcggaggg atctccgtgg ggcggtgaac   300

gccgatgatt atataaggac gcgccgggtg tggcacagct agttccgtcg cagccgggat   360

ttgggtcgcg gttcttgttt gtggatcgct gtgatcgtca cttggtgagt agcgggctgc   420

tgggctggcc ggggctttcg tggccgccgg ccgctcggt gggacggaag cgtgtggaga   480

gaccgccaag ggctgtagtc tgggtccgcg agcaaggttg ccctgaactg ggggttgggg   540

ggagcgcagc aaaatggcgg ctgttcccga gtcttgaatg gaagacgctt gtgaggcggg   600

ctgtgaggtc gttgaaacaa ggtgggggggc atggtgggcg gcaagaaccc aaggtcttga   660

ggccttcgct aatgcgggaa agctcttatt cgggtgagat gggctggggc accatctggg   720

gaccctgacg tgaagtttgt cactgactgg agaactcggt ttgtcgtctg ttgcgggggc   780

ggcagttatg cggtgccgtt gggcagtgca cccgtacctt tgggagcgcg cgccctcgtc   840

gtgtcgtgac gtcacccgtt ctgttggctt ataatgcagg gtggggccac ctgccggtag   900

gtgtgcggta ggcttttctc cgtcgcagga cgcagggttc gggcctaggg taggctctcc   960

```
tgaatcgaca ggcgccggac ctctggtgag gggagggata agtgaggcgt cagtttcttt    1020
```

```
ggtcggtttt atgtacctat cttcttaagt agctgaagct ccggttttga actatgcgct    1080
```

```
cggggttggc gagtgtgttt tgtgaagttt tttaggcacc ttttgaaatg taatcatttg    1140
```

```
ggtcaatatg taattttcag tgttagacta gtaaattgtc cgctaaattc tggccgtttt    1200
```

```
tggctttttt gttagacgaa gcttgg    1226
```

```
<210>    137
<211>    32
<212>    DNA
<213>    Unknown

<220>
<223>    Directional cloning product of Figure 47


<220>
<221>    misc_feature
<222>    (13)..(27)
<223>    N may be any nucleotide

<400>    137
cccttcacca tgnnnnnnnn nnnnnnnaag gg    32


<210>    138
<211>    192
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Cloning region of pLenti6/V5-D-Topo

<400>    138
tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta    60

tataagcaga gctcgtttag tgaaccgtca gatcgcctgg agacgccatc cacgctgttt    120

tgacctccat agaagacacc gactctagag gatccactag tccagtgtgg tggaattgat    180

cccttcacca tg    192


<210>    139
<211>    101
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Cloning region of pLenti6/V5-D-Topo


<220>
<221>    CDS
<222>    (1)..(87)

<400>    139
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aag ggc tcg agt cta gag ggc ccg cgg ttc gaa ggt aag cct atc cct          48
Lys Gly Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro
1               5                   10                  15

aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag taatgagttt          97
Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
            20                  25

ggaa                                                                     101
```

<210> 140
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cloning region of pLenti6/V5-D-Topo

<400> 140

```
Lys Gly Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro
1               5                   10                  15


Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
            20                  25
```

<210> 141
<211> 166
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/V5-DEST

<220>
<221> misc_feature
<222> (166)..(166)
<223> n may be any nucleotide

<400> 141
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caaatgggcg gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact          60

agagaaccca ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa         120

gctggctagt taagctatca acaagtttgt acaaaaaagc aggctn                        166
```

<210> 142
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/V5-DEST

<220>

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<221>  misc_feature
<222>  (4)..(4)
<223>  n may be any nucleotide


<220>
<221>  CDS
<222>  (7)..(108)


<400>  142
tagnac cca gct ttc ttg tac aaa gtg gtt gat cta gag ggc ccg cgg        48
       Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg
       1               5                   10


ttc gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc gat tct acg      96
Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
15              20                  25                  30


cgt acc ggt tag taatgagttt aaacggggga ggctaactga aacacg            144
Arg Thr Gly
```

```
<210>  143
<211>  33
<212>  PRT
<213>  Artificial Sequence


<220>
<223>  Recombination region of pcDNA6.2/V5-DEST


<400>  143

Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe Glu
1               5                   10                  15


Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
            20                  25                  30


Gly
```

```
<210>  144
<211>  166
<212>  DNA
<213>  Artificial Sequence


<220>
<223>  Recombination region of pcDNA6.2/GFP-DEST


<220>
<221>  misc_feature
<222>  (166)..(166)
<223>  n may be any nucleotide


<400>  144
caaatgggcg gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact      60
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agagaaccca ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa   120

gctggctagt taagctatca acaagtttgt acaaaaaagc aggctn   166

<210> 145
<211> 213
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/GFP-DEST

<220>
<221> misc_feature
<222> (4)..(4)
<223> n may be any nucleotide

<220>
<221> CDS
<222> (7)..(213)

<400> 145
tagnac cca gct ttc ttg tac aaa gtg gtt gat cta gag ggc ccc gcg   48
       Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Ala
       1   5   10

gct agc aaa gga gaa gaa ctt ttc act gga ggt gtc cca att ctt gtt   96
Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Gly Val Pro Ile Leu Val
15   20   25   30

gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag   144
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
                35   40   45

ggt gaa ggt gat gct aca tac gga aag ctt acc ctt aaa ttt att tgc   192
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
                50   55   60

act act gga aaa cta cct gtt   213
Thr Thr Gly Lys Leu Pro Val
        65

<210> 146
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/GFP-DEST

<400> 146

Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Ala Ala Ser
1   5   10   15

Lys Gly Glu Glu Leu Phe Thr Gly Gly Val Pro Ile Leu Val Glu Leu
        20   25   30

```
Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
        35                  40                  45


Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
    50                  55                  60


Gly Lys Leu Pro Val
65
```

```
<210>   147
<211>   307
<212>   DNA
<213>   Artificial

<220>
<223>   Recombination region of pAd/CMV/V5 DEST


<220>
<221>   misc_feature
<222>   (172)..(173)
<223>   n is a, c, g, or t

<220>
<221>   CDS
<222>   (176)..(277)

<400>   147
ttgacgcaaa tgggcggtag cgtgtacgg tgggaggtct atataagcag agctctctgg    60

ctaactagag aacccactgc ttactggctt atcgaaatta atacgactca ctatagggag   120

acccaagctg gctagttaag ctatcaacaa gtttgtacaa aaaagcaggc tnnac cca     178
                                                              Pro
                                                              1

gct ttc ttg tac aaa gtg gtt gat cta gag ggc ccg cgg ttc gaa ggt    226
Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe Glu Gly
            5               10              15

aag cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt    274
Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
        20              25              30

tag taatgagttt aaacggggga ggctaactga                                307


<210>   148
<211>   287
<212>   DNA
<213>   Artificial

<220>
<223>   Recombination region of pAd/PL DEST
```

```
<220>
<221>  misc_feature
<222>  (197)..(198)
<223>  n is a, c, g, or t

<400>  148
tatttgtcta gggccgcggg gactttgacc gtttacgtgg agactcgccc aggtgttttt      60

ctcaggtgtt ttccgcgttc cgggtcaaag ttggcgtttt attattatag tcagtcgaag     120

cttggatccg gtacctctag aattctcgag cggccgctag cgacatcgat cacaagtttg     180

tacaaaaaag caggctnnac ccagctttct tgtacaaagt ggtgatcgat tcgacagatc     240

actgaaatgt gtgggcgtgg cttaagggtg ggaaagaata tataagg                  287


<210>  149
<211>  325
<212>  DNA
<213>  Artificial

<220>
<223>  Recombination region of pIB/V5 His DEST


<220>
<221>  misc_feature
<222>  (141)..(142)
<223>  n is a, c, g, or t

<220>
<221>  CDS
<222>  (145)..(276)

<400>  149
cttatcgcgc ctataaatac agcccgcaac gatctggtaa acacagttga acagcatctg      60

ttcgaattta aagcttgata tcgaattcct gcagcccagc gctggatcct cgatcacaag     120

tttgtacaaa aaagcaggct nnac cca cca gct ttc ttg tac aaa gtg gtg       171
                            Pro Pro Ala Phe Leu Tyr Lys Val Val
                            1                5

atc gac ccg ggt cta gag ggc ccg cgg ttc gaa ggt aag cct atc cct     219
Ile Asp Pro Gly Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro
10               15              20                  25

aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt cat cat cac cat     267
Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly His His His His
             30              35                  40

cac cat tga gtttatctga ctaaatctta gttgtattgt catgttttaa tacaatatg   325
His His


<210>  150
<211>  357
<212>  DNA
<213>  Artificial
```

```
<220>
<223>  Recombination region of pLenti6/V5 DEST


<220>
<221>  misc_feature
<222>  (215)..(216)
<223>  n is a, c, g, or t

<220>
<221>  CDS
<222>  (219)..(347)

<400>  150
tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta      60

tataagcaga gctcgtttag tgaaccgtca gatcgcctgg agacgccatc cacgctgttt     120

tgacctccat agaagacacc gactctagag gatccactag tccagtgtgg tggaattctg     180

cagatatcaa caagtttgta caaaaaagca ggctnnac cca gct ttc ttg tac aaa     236
                                            Pro Ala Phe Leu Tyr Lys
                                             1               5

gtg gtt gat atc cag cac agt ggc ggc cgc tcg agt cta gag ggc ccg       284
Val Val Asp Ile Gln His Ser Gly Gly Arg Ser Ser Leu Glu Gly Pro
            10              15                  20

cgg ttc gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc gat tct      332
Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
        25                  30                  35

acg cgt acc ggt tag taatgagttt                                         357
Thr Arg Thr Gly
    40



<210>  151
<211>  359
<212>  DNA
<213>  Artificial

<220>
<223>  Recombination region of the expression clone resulting from
       pLenti6/UbC/V5 DEST x entry clone


<220>
<221>  misc_feature
<222>  (217)..(218)
<223>  n is a, c, g, or t

<220>
<221>  CDS
<222>  (221)..(349)

<400>  151
ttggcgagtg tgttttgtga agttttttag gcaccttttg aaatgtaatc atttgggtca      60

atatgtaatt ttcagtgtta gactagtaaa ttgtccgcta aattctggcc gttttttggct    120
```

```
tttttgttag acgaagcttg gtaccgagct cggatccact agtccagtgt ggtggaattc      180

tgcagatatc aacaagtttg tacaaaaaag caggctnnac cca gct ttc ttg tac       235
                                             Pro Ala Phe Leu Tyr
                                              1               5

aaa gtg gtt gat atc cag cac agt ggc ggc cgc tcg agt cta gag ggc       283
Lys Val Val Asp Ile Gln His Ser Gly Gly Arg Ser Ser Leu Glu Gly
                10              15              20

ccg cgg ttc gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc gat       331
Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp
        25              30              35

tct acg cgt acc ggt tag taatgagttt                                    359
Ser Thr Arg Thr Gly
        40


<210>   152
<211>   293
<212>   DNA
<213>   Artificial

<220>
<223>   Cloning region of pLenti6/V5 D Topo


<220>
<221>   CDS
<222>   (193)..(279)

<400>   152
tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta      60

tataagcaga gctcgtttag tgaaccgtca gatcgcctgg agacgccatc cacgctgttt      120

tgacctccat agaagacacc gactctagag gatccactag tccagtgtgg tggaattgat      180

cccttcacca tg aag ggc tcg agt cta gag ggc ccg cgg ttc gaa ggt aag    231
              Lys Gly Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys
               1               5                      10

cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag      279
Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
    15              20              25

taatgagttt ggaa                                                       293


<210>   153
<211>   310
<212>   DNA
<213>   Artificial

<220>
<223>   Recombination region of pcDNA6.2/V5 DEST


<220>
```

```
<221>  misc_feature
<222>  (166)..(166)
<223>  n is a, c, g, or t


<220>
<221>  misc_feature
<222>  (170)..(170)
<223>  n is a, c, g, or t


<220>
<221>  CDS
<222>  (173)..(274)

<400>  153
caaatgggcg gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact      60

agagaaccca ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa     120

gctggctagt taagctatca acaagtttgt acaaaaaagc aggctntagn ac cca gct     178
                                                             Pro Ala
                                                              1

ttc ttg tac aaa gtg gtt gat cta gag ggc ccg cgg ttc gaa ggt aag     226
Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe Glu Gly Lys
        5                   10                  15

cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag     274
Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
    20                  25                  30

taatgagttt aaacggggga ggctaactga aacacg                               310


<210>  154
<211>  379
<212>  DNA
<213>  Artificial

<220>
<223>  Recombination region of pcDNA6.2/GFP DEST


<220>
<221>  misc_feature
<222>  (166)..(166)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (170)..(170)
<223>  n is a, c, g, or t

<220>
<221>  CDS
<222>  (173)..(379)


<400>  154
caaatgggcg gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact      60

agagaaccca ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa     120
```

```
gctggctagt taagctatca acaagtttgt acaaaaaagc aggctntagn ac cca gct      178
                                                         Pro Ala
                                                           1
```

```
ttc ttg tac aaa gtg gtt gat cta gag ggc ccc gcg gct agc aaa gga      226
Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Ala Ala Ser Lys Gly
         5                   10                  15
```

```
gaa gaa ctt ttc act gga ggt gtc cca att ctt gtt gaa tta gat ggt      274
Glu Glu Leu Phe Thr Gly Gly Val Pro Ile Leu Val Glu Leu Asp Gly
        20                  25                  30
```

```
gat gtt aat ggg cac aaa ttt tct gtc agt gga gag ggt gaa ggt gat      322
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35                  40                  45                  50
```

```
gct aca tac gga aag ctt acc ctt aaa ttt att tgc act act gga aaa      370
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
                    55                  60                  65
```

```
cta cct gtt                                                          379
Leu Pro Val
```

```
<210>   155
<211>   5
<212>   DNA
<213>   Artificial

<220>
<223>   Topoisomerase recognition site


<220>
<221>   misc_feature
<222>   (1)..(1)
<223>   n is c or t

<400>   155
ncctt                                                                    5


<210>   156
<211>   7
<212>   DNA
<213>   Artificial

<220>
<223>   Topoisomerase recognition site for type IA E. coli topoisomerase
        III

<400>   156
gcaactt                                                                  7


<210>   157
<211>   7
<212>   DNA
<213>   Artificial

<220>
```

```
<223>   Overlap region; bases 6-12 in the core region

<400>   157
tttatac                                                                 7


<210>   158
<211>   7
<212>   DNA
<213>   Artificial

<220>
<223>   Consensus sequence


<220>
<221>   misc_feature
<222>   (1)..(3)
<223>   n is a, c, g, or t

<400>   158
nnnatac                                                                 7


<210>   159
<211>   7
<212>   DNA
<213>   Artificial

<220>
<223>   Kozak consensus sequence


<220>
<221>   misc_feature
<222>   (1)..(1)
<223>   n is g or a

<220>
<221>   misc_feature
<222>   (2)..(3)
<223>   n is a, c, g, or t

<400>   159
nnnatgg                                                                 7


<210>   160
<211>   17
<212>   DNA
<213>   Artificial

<220>
<223>   Proposed Reverse PCR primer sequence

<400>   160
tgagctgctg ccacaaa                                                     17


<210>   161
<211>   7
```

```
<212>  DNA
<213>  Artificial

<220>
<223>  Seven base pair inverted repeat region

<400>  161
caacttt                                                                    7


<210>  162
<211>  7
<212>  DNA
<213>  Artificial

<220>
<223>  Seven base pair inverted repeat region

<400>  162
aaagttg                                                                    7


<210>  163
<211>  4
<212>  DNA
<213>  Artificial

<220>
<223>  PCR forward primer addition

<400>  163
cacc                                                                       4


<210>  164
<211>  4
<212>  DNA
<213>  Artificial

<220>
<223>  Overhang in cloning vector

<400>  164
gtgg                                                                       4


<210>  165
<211>  7
<212>  PRT
<213>  Artificial

<220>
<223>  C-terminal polyhistidine tag and free carboxyl group

<220>
<221>  MOD_RES
<222>  (7)..(7)
<223>  Xaa = free carboxyl group


<400>  165
```

```
His His His His His His Xaa
1                   5
```